

The degeneracy code used for the oligonucleotides was as follows: R= A/G; Y=C/T; M=A/C; K=G/T; W=A/T; S=C/G; B=C/G/T; D=A/G/T; H=A/C/T; V=A/C/G; N=A/C/G/T.

REMARKS

Consideration and allowance of the above-referenced application are respectfully requested.

The amendments noted herein reflect the addition of sequence identifier numbers to the application, as filed.

It is believed that the subject application is in condition for allowance and Notice to that effect is respectfully requested.

Should the Examiner have any questions concerning the above, he is respectfully requested to contact the undersigned at the telephone number listed below.



23492

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Respectfully submitted,
Mukerji, et al.

A handwritten signature in cursive script, reading "Cheryl L. Becker".

Cheryl L. Becker
Registration No. 35,441
Attorney for Applicants

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Please amend the subject application as follows:

IN THE SPECIFICATION:

Please amend page 9, line 13 - page 10, line 6 as follows:

Figure 1 is a schematic showing the biosynthetic pathway leading to the production of various PUFAs.

Figure 2 is the nucleotide sequence of *sdd17* (SEQ ID NO: 25), a gene derived from *S. diclina* (ATCC 56851) that encodes a novel ω 3-fatty acid desaturase.

Figure 3 is the amino acid sequence of the ω 3-desaturase (SDD17) (SEQ ID NO: 26) encoded by the nucleotide sequence depicted in Figure 2.

Figure 4 is an amino acid sequence comparison between the SDD17 desaturase (SEQ ID NO: 43) depicted in Figure 3 and a known Δ 15-desaturase from *Synechocystis* sp. (SYCDESB) (SEQ ID NO: 44).

Figure 5 is an amino acid sequence comparison between the SDD17 desaturase (SEQ ID NO: 45) depicted in Figure 3 and a known Δ 17-desaturase from *C. elegans* (CELEFAT) (SEQ ID NO: 46).

Figure 6 is the nucleotide sequence of *sdd12* (SEQ ID NO:41), a gene derived from *S. diclina* (ATCC 56851) that encodes a novel Δ 12-fatty acid desaturase.

Figure 7 is the amino acid sequence of the Δ 12-desaturase (SDD12) (SEQ ID NO: 42) encoded by the nucleotide sequence depicted in Figure 6.

Figure 8 is an amino acid sequence comparison between the SDD12 desaturase (SEQ ID NO: 47) depicted in Figure 7

and a known $\Delta 12$ -desaturase from *G. hirsutum* (GHO6DES) (SEQ ID NO:48).

Figure 9 lists the sequence identifiers used throughout the application as well as the corresponding amino acid or nucleotide sequence.

Please amend page 45, line 12 - page 46, line 30 as follows:

The following degenerate primers were designed and used in various combinations:

Protein Motif 1: NH₃- TRAAIPKHCWVK -COOH
(SEQ ID NO: 49)

Primer RO 1144 (Forward): 5'-ATC CGC GCC GCC ATC CCC
AAG CAC TGC TGG GTC AAG-3' (SEQ ID NO: 1).

Protein Motif 2: NH₃- ALFVLGHDCGHGSFS -COOH
(SEQ ID NO: 50)

This primer contains the histidine-box 1 (underlined).

Primer RO 1119 (Forward): 5'- GCC CTC TTC GTC CTC GGC
CAY GAC TGC GGC CAY GGC TCG TTC TCG-3' (SEQ. ID. NO:
2).

Primer RO 1118 (Reverse): 5'-GAG RTG GTA RTG GGG GAT
CTG GGG GAA GAR RTG RTG GRY GAC RTG-3' (SEQ. ID. NO:
3).

Protein Motif 3: NH₃- PYHGWRISHRTHHQN -COOH
(SEQ ID NO: 51)

This primer contains the histidine-box 2 (underlined).

Primer RO 1121 (Forward): 5'-CCC TAC CAY GGC TGG CGC
ATC TCG CAY CGC ACC CAY CAY CAG AAC-3' (SEQ. ID. NO:
4).

Primer RO 1122 (Reverse): 5'-GTT CTG RTG RTG GGT CCG
RTG CGA GAT GCG CCA GCC RTG GTA GGG-3' (SEQ. ID. NO:
5).

Protein Motif 4: NH₃- GSHF D/H P D/Y SDLFV -COOH
(SEQ ID NO: 52)

Primer RO 1146 (Forward): 5'- GGC TCG CAC TTC SAC CCC
KAC TCG GAC CTC TTC GTC-3' (SEQ. ID. NO: 6).

Primer RO 1147 (Reverse): 5'- GAC GAA GAG GTC CGA GTM
GGG GTW GAA GTG CGA GCC-3' (SEQ. ID. NO: 7).

Protein Motif 5: NH₃- WS Y/F L/V RGGLTT L/I DR -COOH
(SEQ ID NO: 53)

Primer RO 1148 (Reverse): 5'- GCG CTG GAK GGT GGT GAG
GCC GCC GCG GAW GSA CGA CCA-3' (SEQ. ID. NO: 8).

Protein Motif 6: NH₃- HHDIGTHVIHHLFPQ -COOH
(SEQ ID NO: 54)

This sequence contains the third histidine-box
(underlined).

Primer RO 1114 (Reverse): 5'- CTG GGG GAA GAG RTG RTG
GAT GAC RTG GGT GCC GAT GTC RTG RTG-3' (SEQ. ID. NO:
9).

Protein Motif 7: NH₃- H L/F FP Q/K IPHYHL V/I EAT -COOH
(SEQ ID NO: 55)

Primer RO 1116 (Reverse): 5'- GGT GGC CTC GAY GAG RTG
GTA RTG GGG GAT CTK GGG GAA GAR RTG-3' (SEQ. ID. NO:
10).

Protein Motif 8: NH₃- HV A/I HH L/F FPQIPHYHL -COOH

(SEQ ID NO: 56)

This primer contains the third histidine-box (underlined) and accounts for differences between the plant omega-3 desaturases and the *C. elegans* omega-3-desaturase.

Primer RO 1118 (Reverse): 5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3' (SEQ. ID. NO: 11).

The degeneracy code used for SEQ. ID. NOS: 1 through 11 was as follows: R= A/G; Y=C/T; M=A/C; K=G/T; W=A/T; S=C/G; B=C/G/T; D=A/G/T; H=A/C/T; V=A/C/G; and N=A/C/G/T.

Please amend page 65, line 29 - page 66, line 21 with the following:

The degenerate primers used in this Example were as follows:

Protein Motif 1: NH₃- P N/E FTIKEIR D/E A/C IPAHCF - COOH (SEQ ID NO: 57)

Primer RO 967 (Forward): 5'-CCG SAG TTC ACS ATC AAG GAG ATC CGC GAS KSC ATC CCG GCC CAC TGC TTC -3' (SEQ. ID. NO: 30).

Protein Motif 2: NH₃- MP H/F YHAEET V/Y H I/L KK A/L - COOH (SEQ ID NO: 58)

Primer RO 968 (Reverse): 5'-GRS CTT CTT GAK GTG GWM SGT GGC CTC CTC GGC GTG GTA GWR CGG CAT-3' (SEQ. ID. NO: 31).

Protein Motif 3: NH₃- P L/V YW A/I C/M/A QG V/I V L/G/C TGVW -COOH (SEQ ID NO: 59)

Primer RO 964 (Forward): 5'-CCS STC TAC TGG GCC TGC CAG
GGT RTC GTC CTC ACS GGT GTC TGG-3' (SEQ. ID. NO: 32).

This sequence is more similar to the known plant Delta
12-desaturases.

Primer RO 965 (Forward): 5'-CCS STC TAC TGG ATC RYS CAG
GGT RTC GTC KGY ACS GGT GTC TGG-3' (SEQ. ID. NO: 33).

This sequence is more similar to the known fungal Delta
12-desaturases.

Protein Motif 4: NH₃- HVAHH L/F FS T/Q MPHYHA -COOH
(SEQ ID NO: 60)

Primer RO 966 (Reverse): 5'-GGC GTG GTA GTG CGG CAT SMM
CGA GAA GAR GTG GTG GGC GAC GTG-3' (SEQ. ID. NO: 34).

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